RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,874

DATE: 02/22/2001
TIME: 10:35:09

Input Set : A:\Seq.txt
Output Set: N:\CRF3\02222001\I776874.raw

SEQUENCE LISTING

```
 2 (1) GENERAL INFORMATION:
 3        (i) APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
 4                       Feinstein
 5       (ii) TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
 6                       HAVING HEPARANASE ACTIVITY AND EXPRESSION
 7                       OF SAME IN GENETICALLY MODIFIED CELLS
 8      (iii) NUMBER OF SEQUENCES: 47
 9       (iv) CORRESPONDENCE ADDRESS:
10            (A) ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
11            (B) STREET: 2001 Jefferson Davis Highway, Suite 207
12            (C) CITY: Arlington
13            (D) STATE: Virginia
14            (E) COUNTRY: United States of America
15            (F) ZIP: 22202
16        (v) COMPUTER READABLE FORM:
17            (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
18            (B) COMPUTER: Twinhead* Slimnote-890TX
19            (C) OPERATING SYSTEM: MS DOS version 6.2,
20                       Windows version 3.11
21            (D) SOFTWARE: Word for Windows version 2.0 converted to
22                       an ASCI file
23       (vi) CURRENT APPLICATION DATA:
24            (A) APPLICATION NUMBER: US/09/776,874
25            (B) FILING DATE: 06-Feb-2001
26            (C) CLASSIFICATION:
27      (vii) PRIOR APPLICATION DATA:
28            (A) APPLICATION NUMBER: 08/922,170
29            (B) FILING DATE: 2 SEP 1997
30            (A) APPLICATION NUMBER: 09/109,386
31            (B) FILING DATE: 10 JUL 1998
32            (A) APPLICATION NUMBER: PCT/US98/17954
33            (B) FILING DATE: 31 AUG 1998
34     (viii) ATTORNEY/AGENT INFORMATION:
35            (A) NAME: Friedmam, Mark M.
36            (B) REGISTRATION NUMBER: 33,883
37            (C) REFERENCE/DOCKET NUMBER: 910/14
38       (ix) TELECOMMUNICATION INFORMATION:
39            (A) TELEPHONE: 972-3-5625553
40            (B) TELEFAX: 972-3-5625554
41            (C) TELEX:
43 (2) INFORMATION FOR SEQ ID NO: 1:
44        (i) SEQUENCE CHARACTERISTICS:
45            (A) LENGTH: 27
46            (B) TYPE: nucleic acid
47            (C) STRANDEDNESS: single
48            (D) TOPOLOGY: linear
```

C--> 24
C--> 25

RAW SEQUENCE LISTING
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C--> 49   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     50   CCATCCTAAT ACGACTCACT ATAGGGC 27
     52 (2) INFORMATION FOR SEQ ID NO: 2:
     53   (i) SEQUENCE CHARACTERISTICS:
     54   (A) LENGTH: 24
     55   (B) TYPE: nucleic acid
     56   (C) STRANDEDNESS: single
     57   (D) TOPOLOGY: linear
C--> 58   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     59   GTAGTGATGC CATGTAACTG AATC 24
     61 (2) INFORMATION FOR SEQ ID NO: 3:
     62   (i) SEQUENCE CHARACTERISTICS:
     63   (A) LENGTH: 23
     64   (B) TYPE: nucleic acid
     65   (C) STRANDEDNESS: single
     66   (D) TOPOLOGY: linear
C--> 67   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
     68   ACTCACTATA GGGCTCGAGC GGC 23
     70 (2) INFORMATION FOR SEQ ID NO: 4:
     71   (i) SEQUENCE CHARACTERISTICS:
     72   (A) LENGTH: 22
     73   (B) TYPE: nucleic acid
     74   (C) STRANDEDNESS: single
     75   (D) TOPOLOGY: linear
C--> 76   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
     77   GCATCTTAGC CGTCTTTCTT CG 22
     79 (2) INFORMATION FOR SEQ ID NO: 5:
     80   (i) SEQUENCE CHARACTERISTICS:
     81   (A) LENGTH: 15
     82   (B) TYPE: nucleic acid
     83   (C) STRANDEDNESS: single
     84   (D) TOPOLOGY: linear
C--> 85   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
     86   TTTTTTTTTT TTTTT 15
     88 (2) INFORMATION FOR SEQ ID NO: 6:
     89   (i) SEQUENCE CHARACTERISTICS:
     90   (A) LENGTH: 23
     91   (B) TYPE: nucleic acid
     92   (C) STRANDEDNESS: single
     93   (D) TOPOLOGY: linear
C--> 94   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     95   TTCGATCCCA AGAAGGAATC AAC 23
     97 (2) INFORMATION FOR SEQ ID NO: 7:
     98   (i) SEQUENCE CHARACTERISTICS:
     99   (A) LENGTH: 24
     100   (B) TYPE: nucleic acid
     101   (C) STRANDEDNESS: single
     102   (D) TOPOLOGY: linear
C--> 103   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/776,874   TIME: 10:35:09

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```
     104   GTAGTGATGC CATGTAACTG AATC 24
     106  (2) INFORMATION FOR SEQ ID NO: 8:
     107        (i) SEQUENCE CHARACTERISTICS:
     108             (A) LENGTH: 9
     109             (B) TYPE: amino acid
     110             (C) STRANDEDNESS: single
     111             (D) TOPOLOGY: linear
C--> 112       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
     113   Tyr Gly Pro Asp Val Gly Gln Pro Arg
     114                   5               9
     116  (2) INFORMATION FOR SEQ ID NO: 9:
     117        (i) SEQUENCE CHARACTERISTICS:
     118             (A) LENGTH: 1721
     119             (B) TYPE: nucleic acid
     120             (C) STRANDEDNESS: double
     121             (D) TOPOLOGY: linear
C--> 122       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
     123   CTAGAGCTTT CGACTCTCCG CTGCGCGGCA GCTGGCGGGG GGAGCAGCCA GGTGAGCCCA 60
     124   AGATGCTGCT GCGCTCGAAG CCTGCGCTGC CGCCGCCGCT GATGCTGCTG CTCCTGGGGC 120
     125   CGCTGGGTCC CCTCTCCCCT GGCGCCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGG 180
C--> 126   ACCTGGACTT CTTCACCCAG GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCCGTCA 240
     127   CCATTGACGC CAACCTGGCC ACGGACCCGC GGTTCCTCAT CCTCCTGGGT TCTCCAAAGC 300
     128   TTCGTACCTT GGCCAGAGGC TTGTCTCCTG CGTACCTGAG GTTTGGTGGC ACCAAGACAG 360
     129   ACTTCCTAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAGT TACTGGCAAT 420
     130   CTCAAGTCAA CCAGGATATT TGCAAATATG GATCCATCCC TCCTGATGTG GAGGAGAAGT 480
     131   TACGGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
     132   TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAACTGCT 600
     133   CAGGACTGGA CTTGATCTTT GGCCTAAATG CGTTATTAAG AACAGCAGAT TTGCAGTGGA 660
     134   ACAGTTCTAA TGCTCAGTTG CTCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
     135   GGGAACTAGG CAATGAACCT AACAGTTTCC TTAAGAAGGC TGATATTTTC ATCAATGGGT 780
     136   CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAAACTTCT AAGAAAGTCC ACCTTCAAAA 840
     137   ATGCAAAACT CTATGGTCCT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGTGCTGA 900
     138   AGAGCTTCCT GAAGGCTGGT GGAGAAGTGA TTGATTCAGT TACATGGCAT CACTACTATT 960
     139   TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGTATTG GACATTTTTA 1020
     140   TTTCATCTGT GCAAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
     141   GGTTAGGAGA AACAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
     142   CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
     143   TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTT AGTGGATGAA AACTTCGATC 1260
     144   CTTTACCTGA TTATTGGCTA TCTCTTCTGT TCAAGAAATT GGTGGGCACC AAGGTGTTAA 1320
     145   TGGCAAGCGT GCAAGGTTCA AAGAGAAGGA AGCTTCGAGT ATACCTTCAT TGCACAAACA 1380
     146   CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
     147   TCACCAAGTA CTTGCGGTTA CCCTATCCTT TTTCTAACAA GCAAGTGGAT AAATACCTTC 1500
     148   TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAACTCAAT GGTCTAACTC 1560
     149   TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGA AAAACCTCTC CGGCCAGGAA 1620
     150   GTTCACTGGG CTTGCCAGCT TTCTCATATA GTTTTTTTGT GATAAGAAAT GCCAAAGTTG 1680
     151   CTGCTTGCAT CTGAAAATAA AATATACTAG TCCTGACACT G          1721
     153  (2) INFORMATION FOR SEQ ID NO: 10:
     154        (i) SEQUENCE CHARACTERISTICS:
     155             (A) LENGTH: 543
```

```
156              (B) TYPE: amino acid
157              (C) STRANDEDNESS: single
158              (D) TOPOLOGY: linear
C--> 159    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
160  Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
161                       5                 10              15
163  Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
164            .         20              25              30
166  Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
167                 35              40              45
169  Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
170       50              55              60
172  Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
173  65                   70                  75                  80
175  Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
176                 85                  90                  95
178  Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
179            100             105             110
181  Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
182       115             120             125
184  Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
185       130             135             140
187  Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
188  145        .    .   150             155                 160  .
190  Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
191                 165             170             175
193  Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
194            180             185             190
196  Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
197            195             200             205
199  Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
200       210             215             220
202  Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
203  225             230             235                 240
205  Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
206            245             250             255
208  Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
209            260             265             270
211  Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
212       275             280             285
214  Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
215       290             295             300
217  Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
218  305             310             315                 320
220  Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
221            325             330             335
223  Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
224            340             345             350
226  Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
```

```
227        355                360                365
229 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
230     370                375                380
232 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
233 385                390                395                400
235 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
236             405                410                415
238 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
239  ,          420                425                430
241 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
242     435                440                445
244 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
245     450                455                460
247 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
248 465                470                475                480
250 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
251             485                490                495
253 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
254     500                505                510
256 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
257     515                520                525
259 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
260     530                535                540        543
262 (2) INFORMATION FOR SEQ ID NO: 11:
263       (i) SEQUENCE CHARACTERISTICS:
264           (A) LENGTH: 1721
265           (B) TYPE: nucleic acid
266           (C) STRANDEDNESS: double
267           (D) TOPOLOGY: linear
268       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
270                                               CT AGA GCT TTC GAC   14
272 TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG   62
274 ATG CTG CTG CGC TCG AAG CCT GCG CTG CCG CCG CCG CTG ATG CTG CTG  110
275 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
276               5                10                15
278 CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT  158
279 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
280               20                25                30
282 GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC TTC ACC CAG GAG CCG  206
283 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
284               35                40                45
286 CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC  254
287 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
288               50                55                60
290 CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT  302
291 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
292 65                70                75                80
294 CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC  350
295 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/776,874

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Input Set : **A:\Seq.txt**
Output Set: **N:\CRF3\02222001\I776874.raw**

```
L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:58 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:67 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:76 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:85 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:94 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:103 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:112 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:122 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:126 M:111 C: (47) String data converted to upper case,
L:159 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:268 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:418 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:441 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:482 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:480 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=14, Value=[singl]
L:571 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:592 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=15
L:743 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:762 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:771 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:780 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:789 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:798 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:807 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:816 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:825 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:834 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:843 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:852 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:861 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:870 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:879 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:897 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:906 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:915 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:924 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:933 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:942 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:951 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:960 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:969 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:978 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:987 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
```

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PATENT APPLICATION: US/09/776,874

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Input Set : **A:\Seq.txt**
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L:1893 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1917 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=43
L:1949 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2029 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2093 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=45
L:2201 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2217 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]